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RAW SEQUENCE LISTING                      DATE: 02/26/2002
PATENT APPLICATION:  US/09/856,371A       TIME: 09:28:41

          Input Set : A:\sequence listing.txt
          Output Set: N:\CRF3\02262002\I856371A.raw
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 3 <110> APPLICANT: UEMURA, Hidetoshi
 4        OKUI, Akira
 5        KOMINAMI, Katsuya
 6        YAMAGUCHI, Nozomi
 7        MITSUI, Shinichi
 9 <120> TITLE OF INVENTION: NOVEL SERINE PROTEASE BSSP2
11 <130> FILE REFERENCE: UEMURA=7
13 <140> CURRENT APPLICATION NUMBER: 09/856,371A
14 <141> CURRENT FILING DATE: 1999-11-19
16 <150> PRIOR APPLICATION NUMBER: JP 10/347785
17 <151> PRIOR FILING DATE: 1998-11-20
19 <150> PRIOR APPLICATION NUMBER: PCT/JP99/06475
20 <151> PRIOR FILING DATE: 1999-11-19
22 <160> NUMBER OF SEQ ID NOS: 44
24 <170> SOFTWARE: PatentIn version 3.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 717
28 <212> TYPE: DNA
29 <213> ORGANISM: Mus sp.
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(717)
34 <223> OTHER INFORMATION:
37 <400> SEQUENCE: 1
38 ata gtt ggc ggc caa gct gtg gct tct ggg cgc tgg cca tgg caa gct      48
39 Ile Val Gly Gly Gln Ala Val Ala Ser Gly Arg Trp Pro Trp Gln Ala
40  1               5                   10                  15
42 agc gtg atg ctt ggc tcc cgg cac acg tgt ggg gcc tct gtg ttg gca      96
43 Ser Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser Val Leu Ala
44              20                  25                  30
46 cca cac tgg gta gtg act gct gcc cac tgc atg tac agt ttc agg ctg     144
47 Pro His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser Phe Arg Leu
48              35                  40                  45
50 tcc cgc cta tcc agc tgg cgg gtt cat gca ggg ctg gtc agc cat ggt     192
51 Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Gly
52      50                  55                  60
54 gct gtc cga caa cac cag gga act atg gtg gag aag atc att cct cat     240
55 Ala Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile Ile Pro His
56 65                  70                  75                  80
58 cct ttg tac agt gcc cag aac cat gac tat gat gtg gct ctg ctg cag     288
59 Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Gln
60                  85                  90                  95
62 ctc cgg aca cca atc aac ttc tca gac acc gtg gac gct gtg tgc ttg     336
```

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63 Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Asp Ala Val Cys Leu
64         100             105             110
66 ccg gcc aag gag cag tac ttt cca tgg ggg tcg cag tgc tgg gtg tct      384
67 Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys Trp Val Ser
68         115             120             125
70 ggc tgg ggc cac acc gac ccc agc cat act cat agc tca gat aca ctg      432
71 Gly Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser Asp Thr Leu
72         130             135             140
74 cag gac aca atg gta ccc ctg ctc agc acc cac ctc tgc aac agc tca      480
75 Gln Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys Asn Ser Ser
76 145             150             155             160
78 tgc atg tac agt ggg gca ctt aca cac cgc atg ttg tgt gct ggc tac      528
79 Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys Ala Gly Tyr
80             165             170             175
82 ctg gat gga agg gca gac gca tgc cag gga gac agc ggg gga ccc ctg      576
83 Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu
84             180             185             190
86 gta tgt ccc agt ggt gac acg tgg cac ctt gta ggg gtg gtc agc tgg      624
87 Val Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val Val Ser Trp
88         195             200             205
90 ggt cgt ggc tgt gca gag ccc aat cgc cca ggt gtc tat gcc aag gta      672
91 Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr Ala Lys Val
92         210             215             220
94 gca gag ttc ctg gac tgg atc cat gac act gtg cag gtc cgc tag        717
95 Ala Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val Arg
96 225             230             235
99 <210> SEQ ID NO: 2
100 <211> LENGTH: 238
101 <212> TYPE: PRT
102 <213> ORGANISM: Mus sp.
104 <400> SEQUENCE: 2
106 Ile Val Gly Gly Gln Ala Val Ala Ser Gly Arg Trp Pro Trp Gln Ala
107 1               5               10              15
110 Ser Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser Val Leu Ala
111             20              25              30
114 Pro His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser Phe Arg Leu
115         35              40              45
118 Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Gly
119     50              55              60
122 Ala Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile Ile Pro His
123 65              70              75              80
126 Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Gln
127             85              90              95
130 Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Asp Ala Val Cys Leu
131         100             105             110
134 Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys Trp Val Ser
135         115             120             125
138 Gly Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser Asp Thr Leu
139         130             135             140
```

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142 Gln Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys Asn Ser Ser
143 145             150             155             160
146 Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys Ala Gly Tyr
147             165             170             175
150 Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu
151             180             185             190
154 Val Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val Val Ser Trp
155         195             200             205
158 Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr Ala Lys Val
159     210             215             220
162 Ala Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val Arg
163 225             230             235
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 1685
168 <212> TYPE: DNA
169 <213> ORGANISM: Mus sp.
171 <220> FEATURE:
172 <221> NAME/KEY: CDS
173 <222> LOCATION: (247)..(1065)
174 <223> OTHER INFORMATION:
177 <220> FEATURE:
178 <221> NAME/KEY: mat_peptide
179 <222> LOCATION: (352)..()
180 <223> OTHER INFORMATION:
183 <400> SEQUENCE: 3
184 ctcacatgta tctttcagaa taaatggaga ggatcttctg cttcaagtac aagtaagagc      60
186 tcggccagac tggctcctgg tatgccatga gggccggagc ccagccctgg gcatgcacat     120
188 ctgcaagagt cttgggcata tcaggcttac tcaacacaag gccgtgaatc tgtctgacat     180
190 caagctcaac agatcccagg agtttgctca actctctgct agaccgggag gccttgtaga     240
192 ggaggc atg gaa gcc cag gta ggg ctt ctg tgg gtt agc gct aac tgt      288
193        Met Glu Ala Gln Val Gly Leu Leu Trp Val Ser Ala Asn Cys
194         -35             -30             -25
196 cct tct ggc cga att gtt tct ctc aaa tgt tct gag tgt ggg gca agg     336
197 Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu Cys Gly Ala Arg
198    -20             -15             -10
200 cct ctg gct tct cga ata gtt ggc ggc caa gct gtg gct tct ggg cgc     384
201 Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val Ala Ser Gly Arg
202 -5             -1 1             5             10
204 tgg cca tgg caa gct agc gtg atg ctt ggc tcc cgg cac acg tgt ggg     432
205 Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg His Thr Cys Gly
206             15             20             25
208 gcc tct gtg ttg gca cca cac tgg gta gtg act gct gcc cac tgc atg     480
209 Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala Ala His Cys Met
210         30             35             40
212 tac agt ttc agg ctg tcc cgc cta tcc agc tgg cgg gtt cat gca ggg     528
213 Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly
214     45             50             55
216 ctg gtc agc cat ggt gct gtc cga caa cac cag gga act atg gtg gag     576
217 Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly Thr Met Val Glu
```

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Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\02262002\I856371A.raw

```
218 60                      65                  70                  75
220 aag atc att cct cat cct ttg tac agt gcc cag aac cat gac tat gat    624
221 Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp
222               80                  85                  90
224 gtg gct ctg ctg cag ctc cgg aca cca atc aac ttc tca gac acc gtg    672
225 Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val
226               95                  100                 105
228 gac gct gtg tgc ttg ccg gcc aag gag cag tac ttt cca tgg ggg tcg    720
229 Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser
230               110                 115                 120
232 cag tgc tgg gtg tct ggc tgg ggc cac acc gac ccc agc cat act cat    768
233 Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro Ser His Thr His
234               125                 130                 135
236 agc tca gat aca ctg cag gac aca atg gta ccc ctg ctc agc acc cac    816
237 Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu Leu Ser Thr His
238 140                 145                 150                 155
240 ctc tgc aac agc tca tgc atg tac agt ggg gca ctt aca cac cgc atg    864
241 Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met
242               160                 165                 170
244 ttg tgt gct ggc tac ctg gat gga agg gca gac gca tgc cag gga gac    912
245 Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp
246               175                 180                 185
248 agc ggg gga ccc ctg gta tgt ccc agt ggt gac acg tgg cac ctt gta    960
249 Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr Trp His Leu Val
250               190                 195                 200
252 ggg gtg gtc agc tgg ggt cgt ggc tgt gca gag ccc aat cgc cca ggt   1008
253 Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly
254               205                 210                 215
256 gtc tat gcc aag gta gca gag ttc ctg gac tgg atc cat gac act gtg   1056
257 Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Val
258 220                 225                 230                 235
260 cag gtc cgc tagccgaaga agcagcagca gccacctgtg acgccgagct           1105
261 Gln Val Arg
264 gtggatcgcc catggatcac cccagtctgg gggccagcat ctgggtcact gggcctctcc  1165
266 ccaaaggctc tgacttcgag ttcatctttc tcatctgaga acctccacaa caggaaaagg  1225
268 agtctgcggc tagattggga atgatggtga gaggaaggga taggaggaca gaagagacag  1285
270 cagaggcttc tggaagcatc tgggagactg ctcctctgct cccccacac cccacgtgca   1345
272 tccactgggg gatgctggag atgcccaatc cttgtttctt gtggggccac tggaaggcta  1405
274 agtccaactt tagaggatgc cctgtctcga gagttactag gcagataagg ttaaggttgg  1465
276 acaagctcag gtaaaggcac ggaagtcaag atccctctc ccccgtgcgg tcctgttctg   1525
278 aggtaagcta atagccccgc accaggcaga ggtctacagg gtaagaagga tgcagttggg  1585
280 ctacacgacg ctattttca aatgatgttt ctgtaaattg gttgagagag ttttgttatt   1645
282 aaacagaaat tatgtataaa aaaaaaaaa aaaaaaaaa                          1685
285 <210> SEQ ID NO: 4
286 <211> LENGTH: 273
287 <212> TYPE: PRT
288 <213> ORGANISM: Mus sp.
290 <400> SEQUENCE: 4
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293 -35                     -30                    -25                    -20
296 Gly Arg Ile Val Ser Leu Lys Cys Ser Glu Cys Gly Ala Arg Pro Leu
297                     -15                    -10                     -5
300 Ala Ser Arg Ile Val Gly Gly Gln Ala Val Ala Ser Gly Arg Trp Pro
301          -1  1                  5                      10
304 Trp Gln Ala Ser Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser
305      15                  20                     25
308 Val Leu Ala Pro His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser
309 30                  35                     40                     45
312 Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val
313              50                     55                     60
316 Ser His Gly Ala Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile
317              65                     70                     75
320 Ile Pro His Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala
321          80                     85                     90
324 Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Asp Ala
325      95                     100                    105
328 Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys
329 110                 115                    120                    125
332 Trp Val Ser Gly Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser
333              130                    135                    140
336 Asp Thr Leu Gln Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys
337              145                    150                    155
340 Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys
341          160                    165                    170
344 Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly
345      175                    180                    185
348 Gly Pro Leu Val Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val
349 190                 195                    200                    205
352 Val Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr
353              210                    215                    220
356 Ala Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val
357          225                    230                    235
360 Arg
364 <210> SEQ ID NO: 5
365 <211> LENGTH: 2068
366 <212> TYPE: DNA
367 <213> ORGANISM: Mus sp.
369 <220> FEATURE:
370 <221> NAME/KEY: CDS
371 <222> LOCATION: (516)..(1448)
372 <223> OTHER INFORMATION:
375 <220> FEATURE:
376 <221> NAME/KEY: mat_peptide
377 <222> LOCATION: (735)..()
378 <223> OTHER INFORMATION:
381 <400> SEQUENCE: 5
382 ctggctgggc tgttgaatca atcccgacat gaggacagga gcctcaccct gcccagcaga      60
384 acttactgcc ttatatcagt gcagctgact catatgagtc caacactgga tgaccaaagc     120
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VERIFICATION SUMMARY   DATE: 02/26/2002
PATENT APPLICATION: US/09/856,371A   TIME: 09:28:42

Input Set : **A:\sequence listing.txt**
Output Set: **N:\CRF3\02262002\I856371A.raw**

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21